From: Separation Science <elearning.solutions@sepscience.com>
Sent: Thursday, June 21, 2012 1:07 PM
To: Hanchett, James (DPH)
Subject: Read the latest Bruker application notes

Below is a selection of application notes from Bruker. To request full PDFs for any or all of these click on the links below:

AmaZon speed - Improved Speed and Efficiency in Small Molecule LC-MS^n Experiments Using a New Automated Panorama Fragmentation Mode

For the identification and especially the differentiation of structural isomeric compounds MS^n is often mandatory, making ion trap systems the instrument of choice. Here we present new developments implemented with the amaZon speed system enabling fast and efficient MS^n analysis compatible with modern UHPLC and resulting in reproducible, high quality fragmentation spectra.

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Metabolic profiling of Arabidopsis thaliana secondary metabolites using a maXis impact

In this study we profiled metabolite extracts of wild type and mutant Arabidopsis thaliana seedlings impaired in flavonoid biosynthesis. Multivariate data analysis revealed that several compounds were absent in the mutant strains. MS/MS and Pseudo-MS^3 data acquired on a maXis impact high-resolution Q-TOF instrument enabled unambiguous elemental composition determination for precursor and fragment ions.

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Novel approaches for small molecule identification in Metabolomics research

Confirmation of the structure of known compounds and tructural elucidation of unknown compounds represents a bottleneck in the analysis of secondary metabolites in plant metabolomics. The identification of metabolites of interest is an important step for biological interpretation of observed changes in metabolite profiles. In addition, quickly tagging known compounds prevents time being spent repeating their identification.

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Screening for novel natural products from myxobacteria using LC-MS and LC-NMR

Because known pathogens become increasingly resistant to antibiotics, and at the same time, new threats to human health emerge, there is a constant need for the discovery of novel natural products. Microorganisms have a longstanding tradition as a source of biologically active small molecules - termed "secondary metabolites" - and in addition to well-known producers like the actinomycetes, new sources have been established.

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Sensitive Detection of Chloramphenicol in Food

Using the New ionBooster Source with maXis impact. Chloramphenicol (CAP) is a broad-spectrum antibiotic. There is zero-tolerance for its presence in food. Therefore, very sensitive analytical methods are required for accurate, low-level identification and quantitation. To address challenges such as this, we present a new ion source, the ionBooster. In conjunction with high-performance time-of-flight mass spectrometry, the ionBooster enables low-level identification and quantification of target compounds. This application is demonstrated for CAP in beef muscle.

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3,500 Proteins Identified from a Human Cell Lysate Using Complementary MALDI and ESI Data

Recent advances in MS instrumentation and nanoLC separation enable Bruker's ESI and MALDI mass spectrometry platforms to deliver 2,500-3,000 protein IDs from a single sample. Bruker's new solution PRIME enables seamless combination of ESI and MALDI data, increasing sequence coverage and providing significantly enhanced protein identification rates. In this study, merging ESI and MALDI data led to the identification of nearly 3,500 proteins in a human cell lysate.

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